



**Supplemental Figure S2.** Multiple alignment of sequences of the CDA families from *Arabidopsis thaliana* and its close relatives *Arabidopsis lyrata* and *Capsella rubella* from the Camelinaeae tribe.

The genome of *A. thaliana* and its close relatives contain several gene copies coding for potential CDAs. The CDAs which perfectly match the general CDA consensus (Supplemental Figure S1) were placed in the three first rows. The alignment was generated with ClustalW and shaded with Boxshade. Additional shading and labelling as in Supplemental Figure S1. Positions diverging from the general CDA consensus are shaded in yellow. The locus identifiers along the aligned sequences can be found in Supplemental Table S1.